

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/591,432  
Source: IFWP  
Date Processed by STIC: 9/13/06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 09/13/2006

PATENT APPLICATION: US/10/591,432

TIME: 13:16:43

Input Set : N:\RJAVED\10591432.txt

Output Set: N:\CRF4\09132006\J591432.raw

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3 <110> APPLICANT: Frohberg, Claus
4      Koetting, Oliver
5      Ritte, Gerhard
6      Steup, Martin
8 <120> TITLE OF INVENTION: Plants with increased activity of multiple starch
phosphorylating enzymes
10 <130> FILE REFERENCE: 65084.000022
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/591,432
13 <141> CURRENT FILING DATE: 2006-09-01
15 <150> PRIOR APPLICATION NUMBER: EP 04090089.6
16 <151> PRIOR FILING DATE: 2004-03-05
18 <150> PRIOR APPLICATION NUMBER: US 60/550,021
19 <151> PRIOR FILING DATE: 2004-03-05
21 <150> PRIOR APPLICATION NUMBER: EP 04090284.3
22 <151> PRIOR FILING DATE: 2004-07-21
24 <150> PRIOR APPLICATION NUMBER: EP 04090121.7
25 <151> PRIOR FILING DATE: 2004-03-29
27 <160> NUMBER OF SEQ ID NOS: 39
29 <170> SOFTWARE: PatentIn version 3.1
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 3591
33 <212> TYPE: DNA
34 <213> ORGANISM: Arabidopsis thaliana
36 <220> FEATURE:
37 <221> NAME/KEY: CDS
38 <222> LOCATION: (1)..(3591)
39 <223> OTHER INFORMATION:
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45 1          5          10          15
47 act aga aac tca tca tca tca ctt cct aga ctc gtt aac atc act cac      96
48 Thr Arg Asn Ser Ser Ser Ser Leu Pro Arg Leu Val Asn Ile Thr His
49          20          25          30
51 aga gtt aat ctc agc cac caa tct cac cga ctc aga aac tcc aat tct      144
52 Arg Val Asn Leu Ser His Gln Ser His Arg Leu Arg Asn Ser Asn Ser
53          35          40          45
55 cgt ctc act tgc act gct act tct tct tcc acc att gag gaa caa cgg      192
56 Arg Leu Thr Cys Thr Ala Thr Ser Ser Ser Thr Ile Glu Glu Gln Arg
57          50          55          60
59 aag aag aaa gat gga tca gga acg aaa gtg agg ttg aat gtg agg tta      240
60 Lys Lys Lys Asp Gly Ser Gly Thr Lys Val Arg Leu Asn Val Arg Leu
61 65          70          75          80
63 gat cat caa gtt aat ttt ggt gac cat gtg gct atg ttt gga tca gct      288

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64 Asp His Gln Val Asn Phe Gly Asp His Val Ala Met Phe Gly Ser Ala
65                               85                               90                               95
67 aaa gag att ggt tca tgg aaa aag aaa tcg cct ttg aat tgg agt gag      336
68 Lys Glu Ile Gly Ser Trp Lys Lys Lys Ser Pro Leu Asn Trp Ser Glu
69                               100                               105                               110
71 aat gga tgg gtt tgt gag ttg gaa ctt gac ggt ggt cag gtt ttg gag      384
72 Asn Gly Trp Val Cys Glu Leu Glu Leu Asp Gly Gly Gln Val Leu Glu
73                               115                               120                               125
75 tat aag ttt gtc att gtt aag aat gat ggt tca ctt tca tgg gaa tct      432
76 Tyr Lys Phe Val Ile Val Lys Asn Asp Gly Ser Leu Ser Trp Glu Ser
77                               130                               135                               140
79 ggt gat aat cgt gtc ctt aag gtt cca aat tct ggg aat ttt tct gtt      480
80 Gly Asp Asn Arg Val Leu Lys Val Pro Asn Ser Gly Asn Phe Ser Val
81 145                               150                               155                               160
83 gtt tgt cat tgg gat gct act aga gaa acc ctt gat ttg cct cag gag      528
84 Val Cys His Trp Asp Ala Thr Arg Glu Thr Leu Asp Leu Pro Gln Glu
85                               165                               170                               175
87 gtt ggt aat gat gat gat gtt ggt gat ggt ggg cat gag agg gat aat      576
88 Val Gly Asn Asp Asp Asp Val Gly Asp Gly Gly His Glu Arg Asp Asn
89                               180                               185                               190
91 cat gat gtt ggt gat gat aga gta gtg gga agt gaa aat ggt gcg cag      624
92 His Asp Val Gly Asp Asp Arg Val Val Gly Ser Glu Asn Gly Ala Gln
93                               195                               200                               205
95 ctt cag aag agt aca ttg ggt ggg caa tgg caa ggt aaa gat gcg tcc      672
96 Leu Gln Lys Ser Thr Leu Gly Gly Gln Trp Gln Gly Lys Asp Ala Ser
97                               210                               215                               220
99 ttt atg cgt tct aat gat cat ggt aac aga gaa gtt ggt aga aat tgg      720
100 Phe Met Arg Ser Asn Asp His Gly Asn Arg Glu Val Gly Arg Asn Trp
101 225                               230                               235                               240
103 gat act agt ggt ctt gaa ggc aca gct ctt aag atg gtt gag ggt gat      768
104 Asp Thr Ser Gly Leu Glu Gly Thr Ala Leu Lys Met Val Glu Gly Asp
105                               245                               250                               255
107 cgc aac tct aag aac tgg tgg aga aag ctt gaa atg gta cgc gag gtt      816
108 Arg Asn Ser Lys Asn Trp Trp Arg Lys Leu Glu Met Val Arg Glu Val
109                               260                               265                               270
111 ata gtt ggg agt gtt gag agg gag gaa cga ttg aag gcg ctc ata tac      864
112 Ile Val Gly Ser Val Glu Arg Glu Glu Arg Leu Lys Ala Leu Ile Tyr
113                               275                               280                               285
115 tct gca att tat ttg aag tgg ata aac aca ggt cag att cct tgt ttt      912
116 Ser Ala Ile Tyr Leu Lys Trp Ile Asn Thr Gly Gln Ile Pro Cys Phe
117                               290                               295                               300
119 gaa gat gga ggg cat cac cgt cca aac agg cat gcc gag att tcc aga      960
120 Glu Asp Gly Gly His His Arg Pro Asn Arg His Ala Glu Ile Ser Arg
121 305                               310                               315                               320
123 ctt ata ttc cgt gag ttg gag cac att tgc agt aag aaa gat gct act      1008
124 Leu Ile Phe Arg Glu Leu Glu His Ile Cys Ser Lys Lys Asp Ala Thr
125                               325                               330                               335
127 cca gag gaa gtg ctt gtt gct cgg aaa atc cat ccg tgt tta cct tct      1056
128 Pro Glu Glu Val Leu Val Ala Arg Lys Ile His Pro Cys Leu Pro Ser

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133	355				360				365																
135	ata	gcc	cat	cgg	aat	gat	att	cct	cat	gat	ctc	aag	caa	gaa	atc	aag	1152								
136	Ile	Ala	His	Arg	Asn	Asp	Ile	Pro	His	Asp	Leu	Lys	Gln	Glu	Ile	Lys									
137	370				375				380																
139	cat	acg	ata	caa	aat	aag	ctt	cac	cgg	aat	gct	ggg	cca	gaa	gat	cta	1200								
140	His	Thr	Ile	Gln	Asn	Lys	Leu	His	Arg	Asn	Ala	Gly	Pro	Glu	Asp	Leu									
141	385				390				395				400												
143	att	gca	aca	gaa	gca	atg	ctt	caa	cga	att	acc	gag	acc	cca	gga	aaa	1248								
144	Ile	Ala	Thr	Glu	Ala	Met	Leu	Gln	Arg	Ile	Thr	Glu	Thr	Pro	Gly	Lys									
145	405				410				415																
147	tat	agt	gga	gac	ttt	gtg	gag	cag	ttt	aaa	ata	ttc	cat	aat	gag	ctt	1296								
148	Tyr	Ser	Gly	Asp	Phe	Val	Glu	Gln	Phe	Lys	Ile	Phe	His	Asn	Glu	Leu									
149	420				425				430																
151	aaa	gat	ttc	ttt	aat	gct	gga	agt	ctc	act	gaa	cag	ctt	gat	tct	atg	1344								
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153	435				440				445																
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156	Lys	Ile	Ser	Met	Asp	Asp	Arg	Gly	Leu	Ser	Ala	Leu	Asn	Leu	Phe	Phe									
157	450				455				460																
159	gaa	tgt	aaa	aag	cgc	ctt	gac	aca	tca	gga	gaa	tca	agc	aat	gtt	ttg	1440								
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161	465				470				475				480												
163	gag	ttg	att	aaa	acc	atg	cat	tct	cta	gct	tct	tta	aga	gaa	aca	att	1488								
164	Glu	Leu	Ile	Lys	Thr	Met	His	Ser	Leu	Ala	Ser	Leu	Arg	Glu	Thr	Ile									
165	485				490				495																
167	ata	aag	gaa	ctt	aat	agc	ggc	ttg	cga	aat	gat	gct	cct	gat	act	gcc	1536								
168	Ile	Lys	Glu	Leu	Asn	Ser	Gly	Leu	Arg	Asn	Asp	Ala	Pro	Asp	Thr	Ala									
169	500				505				510																
171	att	gca	atg	cgc	cag	aag	tgg	cgc	ctt	tgt	gag	atc	ggc	ctc	gag	gac	1584								
172	Ile	Ala	Met	Arg	Gln	Lys	Trp	Arg	Leu	Cys	Glu	Ile	Gly	Leu	Glu	Asp									
173	515				520				525																
175	tac	ttt	ttt	gtt	cta	cta	agc	aga	ttc	ctc	aat	gct	ctt	gaa	act	atg	1632								
176	Tyr	Phe	Phe	Val	Leu	Leu	Ser	Arg	Phe	Leu	Asn	Ala	Leu	Glu	Thr	Met									
177	530				535				540																
179	gga	gga	gct	gat	caa	ctg	gca	aaa	gat	gtg	gga	tca	aga	aac	gtt	gcc	1680								
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181	545				550				555				560												
183	tca	tgg	aat	gat	cca	cta	gat	gct	ttg	gtg	ttg	ggg	gtt	cac	caa	gta	1728								
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196	Asp	Gly	Lys	Thr	Ile	Trp	Ala	Met	Arg	Leu	Lys	Ala	Thr	Leu	Asp	Arg	
197		610					615				620						
199	gca	cg	aga	tta	aca	gca	gaa	tat	tct	gat	ttg	ctt	ctt	caa	ata	ttt	1920
200	Ala	Arg	Arg	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	Leu	Leu	Leu	Gln	Ile	Phe	
201	625					630				635						640	
203	cct	cct	aat	gtg	gag	att	tta	gga	aaa	gct	cta	gga	att	cca	gag	aat	1968
204	Pro	Pro	Asn	Val	Glu	Ile	Leu	Gly	Lys	Ala	Leu	Gly	Ile	Pro	Glu	Asn	
205				645						650						655	
207	agt	gtc	aag	acc	tat	aca	gaa	gca	gag	att	cgt	gct	gga	att	att	ttc	2016
208	Ser	Val	Lys	Thr	Tyr	Thr	Glu	Ala	Glu	Ile	Arg	Ala	Gly	Ile	Ile	Phe	
209			660						665					670			
211	cag	atc	tca	aag	ctc	tgc	act	gtt	ctt	cta	aaa	gct	gta	aga	aat	tca	2064
212	Gln	Ile	Ser	Lys	Leu	Cys	Thr	Val	Leu	Leu	Lys	Ala	Val	Arg	Asn	Ser	
213			675				680							685			
215	ctt	ggt	tct	gag	ggc	tgg	gat	gtc	gtt	gta	cct	gga	tcg	acg	tct	ggg	2112
216	Leu	Gly	Ser	Glu	Gly	Trp	Asp	Val	Val	Val	Pro	Gly	Ser	Thr	Ser	Gly	
217		690				695					700						
219	aca	tta	gtt	cag	gtt	gag	agc	att	gtt	ccg	gga	tca	ttg	cca	gca	act	2160
220	Thr	Leu	Val	Gln	Val	Glu	Ser	Ile	Val	Pro	Gly	Ser	Leu	Pro	Ala	Thr	
221	705					710				715						720	
223	tct	ggt	ggt	cct	att	att	ctc	ttg	gtc	aat	aaa	gct	gat	ggc	gat	gaa	2208
224	Ser	Gly	Gly	Pro	Ile	Ile	Leu	Leu	Val	Asn	Lys	Ala	Asp	Gly	Asp	Glu	
225				725						730						735	
227	gag	gta	agt	gct	gct	aat	ggg	aac	ata	gct	gga	gtc	atg	ctt	ctg	cag	2256
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229			740					745						750			
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233			755				760							765			
235	att	gtc	ttt	gtg	aca	tgt	gat	gat	gat	gac	aag	gtt	gct	gat	ata	cga	2352
236	Ile	Val	Phe	Val	Thr	Cys	Asp	Asp	Asp	Asp	Lys	Val	Ala	Asp	Ile	Arg	
237		770				775					780						
239	cga	ctt	gtg	gga	aaa	ttt	gtg	agg	ttg	gaa	gca	tct	cca	agt	cat	gtg	2400
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243	aat	ctg	ata	ctt	tca	act	gag	ggt	agg	agt	cg	act	tcc	aaa	tcc	agt	2448
244	Asn	Leu	Ile	Leu	Ser	Thr	Glu	Gly	Arg	Ser	Arg	Thr	Ser	Lys	Ser	Ser	
245				805						810						815	
247	gcg	acc	aaa	aaa	acg	gat	aag	aac	agc	tta	tct	aag	aaa	aaa	aca	gat	2496
248	Ala	Thr	Lys	Lys	Thr	Asp	Lys	Asn	Ser	Leu	Ser	Lys	Lys	Lys	Thr	Asp	
249			820						825					830			
251	aag	aag	agc	tta	tct	atc	gat	gat	gaa	gaa	tca	aag	cct	ggt	tcc	tca	2544
252	Lys	Lys	Ser	Leu	Ser	Ile	Asp	Asp	Glu	Glu	Ser	Lys	Pro	Gly	Ser	Ser	
253			835					840						845			
255	tct	tcc	aat	agc	ctc	ctt	tac	tct	tcc	aag	gat	atc	cct	agt	gga	gga	2592
256	Ser	Ser	Asn	Ser	Leu	Leu	Tyr	Ser	Ser	Lys	Asp	Ile	Pro	Ser	Gly	Gly	
257		850					855					860					
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264	Ala	Ala	Cys	Gly	Leu	Leu	Ala	Ser	Leu	Ala	Glu	Ala	Ser	Ser	Lys	Val	
265					885					890					895		
267	cac	agc	gaa	cac	gga	gtt	ccg	gca	tca	ttt	aag	gtt	cca	act	gga	gtt	2736
268	His	Ser	Glu	His	Gly	Val	Pro	Ala	Ser	Phe	Lys	Val	Pro	Thr	Gly	Val	
269				900					905				910				
271	gtc	ata	cct	ttt	gga	tcg	atg	gaa	tta	gct	tta	aag	caa	aat	aat	tcg	2784
272	Val	Ile	Pro	Phe	Gly	Ser	Met	Glu	Leu	Ala	Leu	Lys	Gln	Asn	Asn	Ser	
273			915					920					925				
275	gaa	gaa	aag	ttt	gcg	tct	ttg	cta	gaa	aaa	cta	gaa	acc	gcc	aga	cct	2832
276	Glu	Glu	Lys	Phe	Ala	Ser	Leu	Leu	Glu	Lys	Leu	Glu	Thr	Ala	Arg	Pro	
277		930					935					940					
279	gag	ggt	ggt	gag	cta	gac	gac	ata	tgt	gac	cag	atc	cat	gaa	gtg	atg	2880
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281	945				950					955					960		
283	aaa	acg	ttg	caa	gtg	cct	aaa	gaa	aca	atc	aac	agc	ata	agc	aaa	gcg	2928
284	Lys	Thr	Leu	Gln	Val	Pro	Lys	Glu	Thr	Ile	Asn	Ser	Ile	Ser	Lys	Ala	
285				965					970					975			
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289			980					985					990				
291	gac	tta	gcc	gga	atg	tca	gct	gca	gga	ctc	tat	gaa	tca	atc	cct	aac	3024
292	Asp	Leu	Ala	Gly	Met	Ser	Ala	Ala	Gly	Leu	Tyr	Glu	Ser	Ile	Pro	Asn	
293			995				1000					1005					
295	gtg	agt	ccc	tcg	gat	cct	ttg	gtg	ttt	tca	gat	tcg	gtt	tgc	caa		3069
296	Val	Ser	Pro	Ser	Asp	Pro	Leu	Val	Phe	Ser	Asp	Ser	Val	Cys	Gln		
297		1010					1015					1020					
299	gtt	tgg	gct	tct	ctc	tac	aca	aga	aga	gct	gtt	cta	agc	cgt	aga		3114
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303	gct	gct	ggt	gtc	tct	caa	aga	gaa	gct	tca	atg	gct	gtt	ctc	gtt		3159
304	Ala	Ala	Gly	Val	Ser	Gln	Arg	Glu	Ala	Ser	Met	Ala	Val	Leu	Val		
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307	caa	gaa	atg	ctt	tcg	ccg	gac	tta	tca	ttc	gtt	ctg	cac	aca	gtg		3204
308	Gln	Glu	Met	Leu	Ser	Pro	Asp	Leu	Ser	Phe	Val	Leu	His	Thr	Val		
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311	agt	cca	gct	gat	ccg	gac	agt	aac	ctt	gtg	gaa	gcc	gag	atc	gct		3249
312	Ser	Pro	Ala	Asp	Pro	Asp	Ser	Asn	Leu	Val	Glu	Ala	Glu	Ile	Ala		
313		1070					1075					1080					
315	cct	ggt	tta	ggt	gag	act	tta	gct	tca	gga	aca	aga	gga	aca	cca		3294
316	Pro	Gly	Leu	Gly	Glu	Thr	Leu	Ala	Ser	Gly	Thr	Arg	Gly	Thr	Pro		
317		1085					1090					1095					
319	tgg	aga	ctc	gct	tcg	ggt	aag	ctc	gac	ggg	att	gta	caa	acc	tta		3339
320	Trp	Arg	Leu	Ala	Ser	Gly	Lys	Leu	Asp	Gly	Ile	Val	Gln	Thr	Leu		
321		1100					1105					1110					
323	gct	ttc	gca	aac	ttc	agc	gaa	gag	ctt	ctt	gtg	tca	gga	aca	ggt		3384
324	Ala	Phe	Ala	Asn	Phe	Ser	Glu	Glu	Leu	Leu	Val	Ser	Gly	Thr	Gly		

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/591,432

DATE: 09/13/2006  
TIME: 13:16:44

Input Set : N:\RJAVED\10591432.txt  
Output Set: N:\CRF4\09132006\J591432.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 8

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/591,432

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Input Set : N:\RJAVED\10591432.txt

Output Set: N:\CRF4\09132006\J591432.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:42 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:39  
L:670 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:667  
L:1321 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:1314  
L:2127 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:2120  
L:2871 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:2864  
L:3665 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:3658  
L:4443 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:4436  
L:5231 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:5224